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Copyright (c) 1993 - 2000 Compugen Ltd
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FEGULT 2 FWCNAB alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C:Species: Gossyplum hirsutum (upland cotton) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change C;Accession: A30838; S06911 R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A;Title: Developmental biochemistry of cottonseed embryogenesis A;Reference number: A30838 A;Accession: A30838 A;Mclecule type: mRNA A;Residues: 1-588 <chl> A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PI A,Experimental source: Var. Coker 201 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.</chl>	Query Match Best Local Similarity 50.0%; Pred. No. 4.2e-05; Matches 20; Conservative 10; Mismatches 10; Indels Qy 2 QEDPQTECQQCQRRCRQQESGPRQQQCQRRCKETCEEEE 41 : :	RESULT 1 \$22477 vicilin precursor - cacao (cacao) C;Species: Theobroma cacao (cacao) C;Accession: \$22477; S22478; S18105; S22050 R;McHenry, L.; Fritz, P.J. Plant Mol. Biol. 18, 1173-1176, 1992 Plant Mol. Biol. 18, 1173-1176, 1992 A;Title: Comparison of the structure and nucleotide sequenc A;Reference number: \$22477; MUID:92288309 A;Accession: \$22478 A;Residues: 1-566 <mch> A;Cross-references: EMBL:X62625 A;Accession: \$22478 A;Cross-references: EMBL:X62625 A;Cross-references: EMBL:X62626 C;Genetics: A;Introns: 211/1; 269/3; 296/3; 391/3; 502/1 C;Superfamily: glycinin C;Keywords: seed: storage protein F;1-24/Domain: signal sequence #status predicted <mat> F;25-566/Product: vicilin #status predicted <mat></mat></mat></mch>	30 65 26.2 911 2 B34721 31 65 26.2 919 2 A39948 32 65 26.2 1306 2 T13592 33 63.5 25.6 33 2 A41822 34 63.5 25.6 51 1 HSMSS1 35 63.5 25.6 51 2 S03997 36 62.5 25.2 342 2 JC7110 37 62 25.0 648 1 JQ1150 38 61 24.6 1390 2 T14004 39 60 24.2 1969 2 T08875 41 60 24.2 1969 2 T08875 41 60 24.2 4957 2 T03454 42 60 24.2 4957 2 T03454 43 59.5 24.0 294 2 T23682 44 59.5 24.0 1282 2 JE0110 45 59 23.8 285 1 I46207
ange 16-Jul-1999	566;	_change 17-Mar-1999	androgen receptor androgen receptor hypothetical prote antimicrobial pept protamine - mouse protamine 1 - rat brain-specific mem protein kinase (EC trfA protein - sli alpha-s2-casein pr histidine kinase h ALR protein - huma ALR protein - huma hypothetical prote glycoprotein A - m involucrin - dog
esis and germination XVIII	ls 0; Gaps 0;	ence of vicilin genes of coco	

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RESULT 3
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alpha-globulin type B precursor (tandem 1) - upland continuous seed storage protein (tandem 1) - upland continuous seed storage protein (species: Gossypium hirsutum (upland cotton) (c; Species: Gossypium hirsutum (upland cotton) (c; Cate: 31-Mar-1990 #sequence_revision 31-Mar-1990 #t (c; Accession: S08059
R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, (c) Accession: S08059
R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, (c) Accession: S08059
R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, (c) Accession: S08059
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A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A;Reference number: S06398
A;Accession: S0691
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein.
C;Superfamily: glycinin
C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
A:Cross-references: EMBL:U80455; PIDN:AAB37887.1; GSPDB:GN00020; CESP:T01D1. A:Experimental Source: strain Bristol N2; clone T01D1 C:Genetics: A:Gene: CESP:T01D1.6 A:Map position: 2
A:Introns: 25/3; 304/3 C:Superfamily: gliadin
                                                                                                                                                                         A;Reference number: Z20623
A;Accession: T29475
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-411 <BRA>
                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T01D1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-509 < CHL>
C; Superfamily: glycinin
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R:Bradshaw, H.; Wohldmann, P.
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A; Accession: S08059
A; Status: not compared with
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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48.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104; DB 2; Pred. No. 0.00084;
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Pred. No. 0.00074;
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hypothetical protein AC3.3 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18592
R;MCMurray, A.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z18995
Вþ
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A; Introns: 18/3
C; Superfamily: gli
                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-425 <WIL>
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted
                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T18592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Date: 31-Mar-1990
C; Accession: S06398
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A; Residues: 1-605 < CHL>
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Best Local :
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315 Q 315
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                                                                                                                         Local Similarity
nes 17; Conser
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17; Conserv
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27.9%;
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Pred. No. 0.19
9; Mismatches
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Pred. No. 0.00
11; Mismatches
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Pred. No.
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protein PV100 [imported] - winter squash C;Species: Cucurbita maxima (winter squash) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T44430 R;Yamada, K.; Shimada, T.; Kondo, M.; Nishimura, M.; Hara-Nishimura, I. J. Biol. Chem. 274, 2563-2570, 1999 A;Title: Multiple functional proteins are produced by cleaving Asn-Gln bonds A;Accession: T44430 A;Accession: T44430 A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving Asn-Gln bonds A;Status: preliminary: translated for the square produced by cleaving A;Status: preliminary: translated for the square produced by cleaving A;Status: preliminary: translated for the square produced by cleaving A;Status: preliminary: translated for the square produced by cleaving A;Status: preliminary: translated for the square produced by cleaving A;Status: preliminary: translated for the square preliminary produced by cleaving A;Status: preliminary preliminar
submitted to the EMBL Data Library, A;Description: The sequence of C. el A;Reference number: Z20704 A;Accession: T29880 A;Status: preliminary; translated fr
                                                                                                                                                        hypothetical protein F19G12.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te.C;Accession: T29880 R;Nhan, M.; Le, T.T.
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A;Residues: 1-810 <YAM>
A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062
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C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Caccession: T18593
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A; Introns: 292/2; 374/3;
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A; Residues: 1-600 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQRGSPRAEYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQ 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.31
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80.5; DB Pred. No. 0.31;
from GB/EMBL/DDBJ
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                                                                                              April
legans
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                                                                                              1996
cosmid F19G12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cleaving Asn-Gln bonds of a singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROOOYCORRCKEICE
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R;Murray, J.; Le, T.T.
R;Murray, May 1996
submitted to the EMBL Data Library, May 1996
submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G. Biosci. Biotechnol. Biochem. 61, 984-988, 1997
A;Title: Primary structure of 6.5k-arginine/glutamate-rich polypeptide A;Reference number: JC5557; MUID:97357433
A;Accession: JC5557
                                                                                                                                                                      C;Genetics:
A;Gene: CESP:F31A3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F31A3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: seed C:Comment: This protein is a storage protein which provides nitrogen and F;12-33,16-29/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arginine/glutamate-rich 6.5K polypeptide - smooth loofah C;Species: Luffa cylindrica (smooth loofah) C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
JC5557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:F19G12.7
A;Map position: X
A;Introns: 18/3
                                                                                                                                                                                                                A;Cross-references: EMBL:U58742; PIDN:AAB36856.1; GSPDB:GN00028; CESP:F31A3.1 A;Experimental source: strain Bristol N2; clone F31A3
                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-242 <M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                     C;Superfamily: ultra-high-sulfur keratin
                                                                                                                            A; Introns: 18/3; 160/3
                                                                                                                                               A; Map position: X
                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                      A; Accession: T29699
                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z20667
                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T29699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-47 < KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: JC5557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U51997; PIDN:AAC48159.1; GSPDB:GN00028; CESP:F19G12.7 A;Experimental source: strain Bristol N2; clone F19G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-572 <NHA>
                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 QCQQCQNTCQQFAPVCEQQCASLCHQPSAPQCQQ-CQNTCQQFAPVCEQQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PRTEYEACRVRCQVAEHGVER----QRRCQQVCEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 ECQQCQRRCRQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 POTECOOCORRCROOESGPROOOYCORRCKEICEE
                                                                                                                                                                                                                                                            1-242 <MUR>
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                      31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QESGPRQQQYCQRRCKE---ICEEE 40
Score 77.5; D
Pred. No. 0.26
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78; DB 2; Pred. No. 0.07; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 79; DB 2
Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                cosmid F31A3
                      . 26;
                                          DВ
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                                       Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Conservative

12;

Indels

11;

Gaps

4

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C:Accession: T31888
R:Greco, T.; Bradshaw, H.; Elliott, G.
R:Greco, T.; Bradshaw, H.; Elliott, G.
submitted to the EMBL Data Library, July 1997
submitted to the enumber of C. elegans cosmid C03A7.
A:Reference number: Z21096
hypothetical protein C03A7.8 - C; Species: Caenorhabditis elega
                                                                                                                                                                                                                                                                                                                              A; Introns: 75/3
C; Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-388 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C03A7.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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A;Residues: 1-388 <GRE>
A;Cross-references: EMBL:AF016451; PIDN:AAB66001.1; GSPDB:GN00023; CESP:C03A7.4
A;Experimental source: strain Bristol N2; clone C03A7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Greco, T.: Bradshaw, H.: Elliott, G. submitted to the EMBL Data Library, July 1997 A:Description: The sequence of C. elegans cosmid C03A7. A:Reference number: Z21096 A:Accession: T31887
                                           T31889
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF016451; PIDN:AAB65996.1; GSPDB:GN00023; CESP:C03A7.7 A;Experimental source: strain Bristol N2; clone C03A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T31888
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A; Introns: 75/3
C; Superfamily: gliadin
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C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
C:Accession: T31887
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                                                               RESULT
                                                                                                                                 В
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                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                             191 QQAQAQCQPQCQQQCQSSCVQQQQQSNQCEPACNTQCSDICQQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 QQAQAQCQPQCQQQCQSSCVQQQQQQSNQCEPACNTQCSDICQQ 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 EDPQTECQ-QCQRRC-----RQQESGPRQQQYCQRRCKEICEE 39
                                                                                                                                                                        3 EDPQTECQ-QCQRRC-----RQQESGPRQQQYCQRRCKEICEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                        29.8%; Score 74; DB 2; 30.2%; Pred. No. 0.84;
elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%; Score 74; DB 2; Length 388; 30.2%; Pred. No. 0.84;
                  Caenorhabditis elegans
                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                              Length 388
                                                                                                                                                                             39
                                                                                                                                                                                                                     Indels
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Search completed: March Job time: 543 sec

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A; Map position:
A; Introns: 75/3
C; Superfamily: 9
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A; Introns: 18/3; 75/3
C; Superfamily: gliadin
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R;Greco. T; Bradshaw, H.; Elliott, G.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C03A7.
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                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBCA;Molecule type: DNAA;Residues: 1-445 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid CO3A7
A;Reference number: Z21096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C03A7.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T31898
                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF016451; PIDN:AAB66007.1; GSPDB:GN00023; CESP:C03A7.14
A;Experimental source: strain Bristol N2; clone C03A7
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A;Gene: CESP:C03A7.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-438 <GRE>
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A; Accession: T31889
                                                                                                                                                                                                                                                  A; Gene: CESP: C03A7.14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                  Matches
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Best Local (
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191 QQAQAQCQPQCQQQCQSSCVQQQQPSTQCEPACNTQCSDICQQ
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                                                                                Local Similarity 30.2 hes 13; Conservative
                                         3 EDPOTECO-OCORRC-----ROOESGPROOOYCORRCKEICEE 39
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Pred. No. 0.92
12; Mismatches
                                                                                                   Score 74; DB 2;
Pred. No. 0.93;
                                                                                  Mismatches
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    233
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